

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:19:49 ; Search time 1699 Seconds
(without alignments)
669.140 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20
Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

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9: gb_ro.*
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	21	6	CQ799983 Sequence
3	19	95.0	19	6	CQ799992 Sequence
4	16	80.0	21	6	CQ799905 Sequence
5	15	75.0	21	6	CQ799906 Sequence
6	14.2	71.0	33	6	AR559501 Sequence
7	14.2	71.0	33	6	AX473165 Sequence
8	13.8	69.0	42	6	AR041097 Sequence
9	13.8	69.0	42	6	AR060705 Sequence
10	13.8	69.0	42	6	AR063138 Sequence
11	13.8	69.0	42	6	AR117027 Sequence
12	13.8	69.0	42	6	I64789 Sequence 14
13	13.2	66.0	27	6	E41696 Process for
14	13.2	66.0	43	6	AX496977 Sequence
15	13.2	66.0	43	6	AX703486 Sequence
16	13.2	66.0	43	6	AX720926 Sequence
17	13.2	66.0	43	6	AX925315 Sequence
18	13.2	66.0	43	6	AX925574 Sequence

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c 21	12.8	64.0	23	6	AX034952	AX034952	Sequence
c 22	12.8	64.0	24	6	AX684030	AX684030	Sequence
c 23	12.8	64.0	37	6	AR379389	AR379389	Sequence
c 24	12.8	64.0	40	6	AR053662	AR053662	Sequence
c 25	12.8	64.0	40	6	AR053704	AR053704	Sequence
c 26	12.8	64.0	40	6	AR258597	AR258597	Sequence
c 27	12.8	64.0	40	6	AR258639	AR258639	Sequence
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c 31	12.6	63.0	24	6	AR628409	AR628409	Sequence
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c 33	12.6	63.0	30	6	AR363940	AR363940	Sequence
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c 35	12.6	63.0	37	6	A10006	A10006	Nucleotide
c 36	12.6	63.0	39	6	AR092584	AR092584	Sequence
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c 38	12.6	63.0	42	6	BD141508	BD141508	Method fo
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c 42	12.6	63.0	50	6	AX960395	AX960395	Sequence
c 43	12.4	62.0	20	6	AR014592	AR014592	Sequence
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ALIGNMENTS

RESULT 1

CQ799984

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CQ799984 20 bp DNA linear PAT 28-APR-2004
Sequence 82 from Patent WO2004030660.

CQ799984.1 GI:46848931

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1

Gleave, M.E., Rocchi, P. and Signaevsky, M.

Compositions for treatment of prostate and other cancers

Patent: WO 2004030660-A 82 15-APR-2004;

The University of British Columbia (CA)

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

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CQ799983

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

CQ799983 21 bp DNA linear PAT 28-APR-2004
Sequence 81 from Patent WO2004030660.

CQ799983.1 GI:46848930

Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
JOURNAL Location/Qualifiers
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Db 2 GGGACGGCGCTCGGTTCAT 21
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DEFINITION Sequence 90 from Patent WO2004030660.
ACCESSION CQ799992
VERSION CQ799992.1 GI:46848939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 90 15-APR-2004;
The University of British Columbia (CA)
JOURNAL Location/Qualifiers
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LOCUS 21 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 3 from Patent WO2004030660.
ACCESSION CQ799905
VERSION CQ799905.1 GI:46848852
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
JOURNAL Location/Qualifiers
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Db 1 CGCGCGCTCGGTTCAT 16
RESULT 5
CQ799906
LOCUS 21 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 4 from Patent WO2004030660.
ACCESSION CQ799906
VERSION CQ799906.1 GI:46848853
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 4 15-APR-2004;
The University of British Columbia (CA)
JOURNAL Location/Qualifiers
FEATURES source
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/db_xref="taxon:9606"
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Db 7 GGGACGGCGCTCG 21
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AR559501
LOCUS 33 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 16 from patent US 6750042.
ACCESSION AR559501
VERSION AR559501.1 GI:53968947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Summers, A.O. and Cagliati, J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
FEATURES source
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JOURNAL Patent: WO 2004030660-A 3 15-APR-2004;
The University of British Columbia (CA)
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Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CGCGCGCTCGGTTCAT 20
Db 1 CGCGCGCTCGGTTCAT 16
RESULT 5
CQ799906
LOCUS 21 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 4 from Patent WO2004030660.
ACCESSION CQ799906
VERSION CQ799906.1 GI:46848853
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 4 15-APR-2004;
The University of British Columbia (CA)
JOURNAL Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCGCTCG 15
Db 7 GGGACGGCGCTCG 21
RESULT 6
AR559501
LOCUS 33 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 16 from patent US 6750042.
ACCESSION AR559501
VERSION AR559501.1 GI:53968947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Summers, A.O. and Cagliati, J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
FEATURES source
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Qy 1 GGGACGGCGCTCGGTCA 19
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Db 6 GGGTCTCGGCTCGGGCA 24

RESULT 7
AX473165
LOCUS AX473165
DEFINITION Sequence 16 from Patent WO230962.
ACCESSION AX473165
VERSION AX473165.1 GI:22207875
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Summers,A.O. and Caguiat,J.J.
AUTHORS Metal binding proteins, recombinant host cells and methods
TITLE Patent: WO 0230962-A 16 18-APR-2002;
JOURNAL UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
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Db 6 GGGTCTCGGCTCGGGCA 24

RESULT 8
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LOCUS AR041097
DEFINITION Sequence 21 from patent US 5811264.
ACCESSION AR041097
VERSION AR041097.1 GI:5961593
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Aitken,J.F., Apostol,I.Z., Lippincott,J.A. and Levine,J.D.
TITLE Proteins with mutations to decrease N-terminal methylation
JOURNAL Patent: US 5811264-A 21 22-SEP-1998;
FEATURES Location/Qualifiers
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Qy 4 ACGCGCGCTCGGTCA 20
|||||
Db 16 ACGTCTCGGCTCGGTCT 32

RESULT 9
AR060705
LOCUS AR060705
DEFINITION Sequence 14 from patent US 5840851.
ACCESSION AR060705
VERSION AR060705.1 GI:5987155
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Plomer,J.Jeffrey., Ryland,J.R., Matthews,M.-A.H., Traylor,D.W.,
Milne,E.E., Durfee,S.L., Mathews,A.J. and Neway,J.O.
TITLE Purification of hemoglobin
JOURNAL Patent: US 5840851-A 14 24-NOV-1998;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 42;
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Qy 4 ACGCGCGCTCGGTCA 20
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Db 16 ACGTCTCGGCTCGGTCT 32

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AR063138
LOCUS AR063138
DEFINITION Sequence 17 from patent US 5844090.
ACCESSION AR063138
VERSION AR063138.1 GI:5990829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Anderson,D.C., Mathews,A.J., Trimble,S.P. and Anthony-Cahill,S.
TITLE Modified hemoglobin-like compounds
JOURNAL Patent: US 5844090-A 17 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..42
/organism="unknown"
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ORIGIN

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Db 16 ACGTCTCGGCTCGGTCT 32

RESULT 11
AR117027
LOCUS AR117027
DEFINITION Sequence 21 from patent US 6140071.
ACCESSION AR117027
VERSION AR117027.1 GI:14097933
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Aitken,J.F., Apostol,I.Z., Lippincott,J.A. and Levine,J.D.
TITLE Proteins with mutations to decrease N-terminal methylation
JOURNAL Patent: US 6140071-A 21 31-OCT-2000;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

ACCESSION AR060705
VERSION AR060705.1 GI:5987155
KEYWORDS
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ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Plomer,J.Jeffrey., Ryland,J.R., Matthews,M.-A.H., Traylor,D.W.,
Milne,E.E., Durfee,S.L., Mathews,A.J. and Neway,J.O.
TITLE Purification of hemoglobin
JOURNAL Patent: US 5840851-A 14 24-NOV-1998;
FEATURES Location/Qualifiers
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ORIGIN

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Qy 4 ACGCGCGCTCGGTCA 20
|||||
Db 16 ACGTCTCGGCTCGGTCT 32

RESULT 10
AR063138
LOCUS AR063138
DEFINITION Sequence 17 from patent US 5844090.
ACCESSION AR063138
VERSION AR063138.1 GI:5990829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Anderson,D.C., Mathews,A.J., Trimble,S.P. and Anthony-Cahill,S.
TITLE Modified hemoglobin-like compounds
JOURNAL Patent: US 5844090-A 17 01-DEC-1998;
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DEFINITION Sequence 21 from patent US 6140071.
ACCESSION AR117027
VERSION AR117027.1 GI:14097933
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Aitken,J.F., Apostol,I.Z., Lippincott,J.A. and Levine,J.D.
TITLE Proteins with mutations to decrease N-terminal methylation
JOURNAL Patent: US 6140071-A 21 31-OCT-2000;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: December 13, 2005, 13:58:20
Job time : 1701 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 08:34:39 ; Search time 260 Seconds
(without alignments)
512.669 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggagcggcgctcggtcat 20

Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 4879314

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
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22	13.2	66.0	43	8	ACC69259	Acc69259 Rep68 and	
23	13.2	66.0	43	10	ADI40307	Adi40307 Rep68 and	
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25	13.2	66.0	43	10	ABX96538	Abx96538 Rep68 and	
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27	13.2	66.0	49	2	AAT80499	Aat80499 Hepatoma	
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c	35	12.8	64.0	39	6	ABA98226	AbA98226 Oligonucl
36	12.8	64.0	40	2	AAT69484	Aat69484 Plasmid p	
c	37	12.8	64.0	40	2	AAT69525	Aat69525 Plasmid p
c	38	12.8	64.0	40	2	AAV51220	Aav51220 Maize pol
39	12.8	64.0	40	2	AAx88908	Aax88908 Circular	
c	40	12.8	64.0	40	2	AAx88950	Aax88950 Circular
41	12.8	64.0	40	6	ABA98183	AbA98183 Oligonucl	
42	12.8	64.0	40	6	ABA98184	AbA98184 Oligonucl	
c	43	12.8	64.0	41	6	ABV75699	Abv75699 Human zin
c	44	12.8	64.0	42	14	AEb08695	Aeb08695 RSV-X low
45	12.8	64.0	44	14	AEb08694	Aeb08694 RSV-X low	

ALIGNMENTS

RESULT 1

ADM94732
ID ADM94732 standard; DNA; 20 BP.

AC ADM94732;

DT 01-JUL-2004 (first entry)

XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.

XX heat shock protein 27; hsp27; cytosstatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW antisense oligonucleotide; ss.

XX Homo sapiens.

OS Synthetic.

PN WO2004030660-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

XX 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous system malignancy.

XX Claim 6; SEQ ID NO 82; 38pp; English.

XX The present invention describes a composition which comprises a therapeutic agent that reduces the amount of active heat shock protein 27 (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The

CC composition has cytostatic activity, and can be used in gene therapy. The
 CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
 CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
 CC cancer or a central nervous system malignancy. The present sequence
 CC represents a human hsp27 antisense oligonucleotide which is used in the
 CC exemplification of the present invention.

SQ Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
 |||||
 DB 1 GGGACGGCGGCTCGGTTCAT 20

RESULT 2

ADM94731
 ID ADM94731 standard; DNA; 21 BP.

XX
 AC ADM94731;

XX
 DT 01-JUL-2004 (first entry)

XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.

XX heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW antisense oligonucleotide; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX
 FN 15-APR-2004.

XX
 PF 02-OCT-2003; 2003WO-CA001588.

XX
 PR 02-OCT-2002; 2002US-0415859P.

XX
 PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of
 PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
 PT useful in treating cancer, e.g., prostate cancer or a central nervous
 PT system malignancy.

XX Claim 5; SEQ ID NO 81; 38pp; English.

XX The present invention describes a composition which comprises a
 CC therapeutic agent that reduces the amount of active heat shock protein 27
 CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
 CC composition has cytostatic activity, and can be used in gene therapy. The
 CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
 CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
 CC cancer or a central nervous system malignancy. The present sequence
 CC represents a human hsp27 antisense oligonucleotide which is used in the
 CC exemplification of the present invention.

SQ Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
 |||||
 DB 2 GGGACGGCGGCTCGGTTCAT 21

RESULT 3

ADM94740/c
 ID ADM94740 standard; DNA; 19 BP.

XX
 AC ADM94740;

XX
 DT 01-JUL-2004 (first entry)

XX Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.

XX heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW short interfering RNA; siRNA; RNA interference; RNAi; ds.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX
 FN 15-APR-2004.

XX
 PF 02-OCT-2003; 2003WO-CA001588.

XX
 PR 02-OCT-2002; 2002US-0415859P.

XX
 PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of
 PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
 PT useful in treating cancer, e.g., prostate cancer or a central nervous
 PT system malignancy.

XX Claim 10; SEQ ID NO 90; 38pp; English.

XX The present invention describes a composition which comprises a
 CC therapeutic agent that reduces the amount of active heat shock protein 27
 CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
 CC composition has cytostatic activity, and can be used in gene therapy. The
 CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
 CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
 CC cancer or a central nervous system malignancy. The present sequence
 CC represents a human hsp27 short interfering RNA (siRNA) oligonucleotide
 CC which is used in the exemplification of the present invention.

XX Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTTCAT 20
 |||||
 DB 19 GGACGGCGGCTCGGTTCAT 1

RESULT 4

ADM94653
 ID ADM94653 standard; DNA; 21 BP.

XX
 AC ADM94653;

XX
 DT 01-JUL-2004 (first entry)

XX


```

DE XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3.
KW KW heat shock protein 27; hsp27; cytostatic; gene therapy;
KW KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
XX KW antisense oligonucleotide; ss.
OS OS Homo sapiens.
OS OS Synthetic.
PN PN WO2004030660-A2.
XX XX
XX PD 15-APR-2004.
XX XX
XX PF 02-OCT-2003; 2003WO-CA001588.
XX XX
PR 02-OCT-2002; 2002US-0415859P.
PR 18-APR-2003; 2003US-0463952P.
XX XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX XX
PI Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX XX
XX PD New composition comprising a therapeutic agent that reduces the amount of
XX PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
XX PT useful in treating cancer, e.g., prostate cancer or a central nervous
XX PT system malignancy.
XX PS Claim 5; SEQ ID NO 3; 38pp; English.
XX CC The present invention describes a composition which comprises a
XX CC therapeutic agent that reduces the amount of active heat shock protein 27
XX CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
XX CC composition has cytostatic activity, and can be used in gene therapy. The
XX CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
XX CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
XX CC cancer or a central nervous system malignancy. The present sequence
XX CC represents a human hsp27 antisense oligonucleotide which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 80.0%; Score 16; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 8.2e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CGCGGCGCTCGGTCAAT 20
Db 1 CGCGGCGCTCGGTCAAT 16
XX
RESULT 5
ADN94654
ID ADN94654 standard; DNA; 21 BP.
XX
XX AC ADN94654;
XX XX
XX DT 01-JUL-2004 (first entry)
XX XX
XX DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.
XX KW heat shock protein 27; hsp27; cytostatic; gene therapy;
XX KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
XX KW antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004030660-A2.
XX XX
XX PD 15-APR-2004.
XX XX
XX PF 02-OCT-2003; 2003WO-CA001588.
XX XX
PR 02-OCT-2002; 2002US-0415859P.
PR 18-APR-2003; 2003US-0463952P.
XX XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX XX
PI Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX XX
XX PD New composition comprising a therapeutic agent that reduces the amount of
XX PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
XX PT useful in treating cancer, e.g., prostate cancer or a central nervous
XX PT system malignancy.
XX PS Claim 5; SEQ ID NO 3; 38pp; English.
XX CC The present invention describes a composition which comprises a
XX CC therapeutic agent that reduces the amount of active heat shock protein 27
XX CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
XX CC composition has cytostatic activity, and can be used in gene therapy. The
XX CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
XX CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
XX CC cancer or a central nervous system malignancy. The present sequence
XX CC represents a human hsp27 antisense oligonucleotide which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 80.0%; Score 16; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 8.2e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CGCGGCGCTCGGTCAAT 20
Db 1 CGCGGCGCTCGGTCAAT 16
XX
RESULT 5
ADN94654
ID ADN94654 standard; DNA; 21 BP.
XX
XX AC ADN94654;
XX XX
XX DT 01-JUL-2004 (first entry)
XX XX
XX DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.
XX KW heat shock protein 27; hsp27; cytostatic; gene therapy;
XX KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
XX KW antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004030660-A2.
XX XX
XX PD 15-APR-2004.
XX XX
XX PF 02-OCT-2003; 2003WO-CA001588.
XX PR 02-OCT-2002; 2002US-0415859P.
XX PR 18-APR-2003; 2003US-0463952P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX XX
XX PD New composition comprising a therapeutic agent that reduces the amount of
XX PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
XX PT useful in treating cancer, e.g., prostate cancer or a central nervous
XX PT system malignancy.
XX PS Claim 5; SEQ ID NO 4; 38pp; English.
XX CC The present invention describes a composition which comprises a
XX CC therapeutic agent that reduces the amount of active heat shock protein 27
XX CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
XX CC composition has cytostatic activity, and can be used in gene therapy. The
XX CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
XX CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
XX CC cancer or a central nervous system malignancy. The present sequence
XX CC represents a human hsp27 antisense oligonucleotide which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 15; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGACGCGGCGCTCG 15
Db 7 GGGACGCGGCGCTCG 21
XX
RESULT 6
ABK52211
ID ABK52211 standard; DNA; 33 BP.
XX
XX AC ABK52211;
XX DT 13-AUG-2002 (first entry)
XX DE Synthetic product 2 reverse PCR primer for construction of PASK-MBD.
XX KW Mercuric ion; contaminated soil; ground water; hydroponic solution;
XX KW irrigation water; waste stream; contaminated aqueous medium;
XX KW biological fluid; gastrointestinal tract; chelon protein;
XX KW enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
XX KW heavy metal binding protein; PASK-MBD; PCR; primer; ss.
XX OS Synthetic.
XX OS WO200230962-A2.
XX PN 18-APR-2002.
XX PD
XX XX
XX PF 12-OCT-2001; 2001WO-US031819.
XX PR 12-OCT-2000; 2000US-0240465P.
XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX PI Summers AO, Caguiat JJ;
XX WPI; 2002-435437/46.
XX XX
XX PT Novel non-naturally occurring recombinant DNA molecule encoding a chelon
XX PT protein useful for binding divalent cation mercury from contaminated

```

PT soil, water, aqueous medium including biological fluids.
 XX Disclosure; Page 24; 42pp; English.
 PS
 XX
 CC The present invention relates to a new non-naturally occurring
 CC recombinant DNA molecule comprising a sequence encoding a chelon protein
 CC which binds mercuric ions. The invention is useful for recombinantly
 CC producing a protein in a host-cell, by infecting or transforming a host
 CC cell capable of expressing a chelon coding sequence with a vector
 CC comprising a promoter active in the host cell operably linked to a coding
 CC region for the protein to produce a recombinant host cell and culturing
 CC the recombinant host cell under conditions, where DNA is expressed. The
 CC nucleic acid encoding the chelon protein is useful for binding divalent
 CC mercuric ions, to take up, sequester and concentrate the heavy metal ions
 CC from contaminated soil, ground water, hydroponic solutions or irrigation
 CC water of waste streams. The DNA of the invention, when immobilised onto a
 CC solid support, is useful for concentrating heavy metal ions from
 CC contaminated environment waste streams or contaminated aqueous medium
 CC including biological fluids. The nucleic acid, when recombinantly
 CC expressed in enteric bacteria (which are nontoxic and nonpathogenic),
 CC is suitable for use in the in vivo sequestration and elimination of
 CC mercuric ion from gastrointestinal tracts of animals or humans exposed to
 CC toxic metal ions such as mercury and/or cadmium. The molecules of the
 CC invention are also useful in water treatment resins. The nucleic acid of
 CC the invention is highly specific and binds divalent cation such as
 CC mercury or cadmium with high affinity. The present nucleic acid sequence
 CC represents synthetic product 2 reverse PCR primer that was used in the
 CC methods of the invention for construction of pASK-MED vector
 XX
 SQ Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;
 Query Match 71.0%; Score 14.2; DB 6; Length 33;
 Best Local Similarity 84.2%; Pred. No. 5.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGACGCGCGCTCGGTCA 19
 ||| ||||| ||||| ||
 Db 6 GGGTCTCGGCGCTCGGCCA 24
 RESULT 7
 ABZ68928/c
 ID ABZ68928 standard; DNA; 47 BP.
 XX
 AC ABZ68928;
 XX
 XX 28-MAY-2003 (first entry)
 DE
 DE PCR primer used to amplify a PKS domain DNA sequence.
 XX
 KW Simvastatin; polyketide synthase; PKS; HMPKSB2; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO2003010324-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 25-JUL-2002; 2002WO-IN000157.
 XX
 PR 25-JUL-2001; 2001IN-DE000796.
 XX
 PA (ITGB-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
 XX
 PI Ranganathan A;
 XX
 DR WPI; 2003-248083/24.
 XX
 XX Preparing simvastatin or its analogs or derivatives, by providing a host
 PT having a customized gene encoding a polyketide synthase, and fermenting
 PT the host to obtain simvastatin or its analogs or derivatives.
 XX
 PS Example 1.2.3; Page 21; 40pp; English.

XX The specification describes a method of preparing simvastatin or its
 CC analogues or derivatives by biological expression. The method comprises
 CC providing a host having a customized gene encoding for a polyketide
 CC synthase (PKS), and fermenting the host to obtain simvastatin or its
 CC analogues or derivatives. The method is useful for producing simvastatin
 CC or its analogues or derivatives. PCR primers ABZ68927-28 were used to
 CC amplify a PKS domain DNA sequence. The amplified fragment was used in the
 CC construction of the hybrid modular PKS B2 (HMPKSB2), for use in the
 CC method of the invention
 XX
 SQ Sequence 47 BP; 8 A; 14 C; 20 G; 5 T; 0 U; 0 Other;
 Query Match 71.0%; Score 14.2; DB 8; Length 47;
 Best Local Similarity 84.2%; Pred. No. 5.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGACGCGCGCTCGGTCA 19
 ||| ||||| ||||| ||
 Db 33 GGACCGCGCGCTCGGCCA 15
 RESULT 8
 ACH58106
 ID ACH58106 standard; DNA; 25 BP.
 XX
 AC ACH58106;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 XX DNA target sequence #7242 useful in array for genetic analyses.
 DE
 DE Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;
 KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Mittmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 XX New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 7242; 9pp; English.
 XX
 XX The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA

CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH5260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdIDEntry.html
 XX
 SQ Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGCGCGCTCG 15
 Db 2 GGACGCGCGCTCG 15

RESULT 9
 AAQ87144
 ID AAQ87144 standard; DNA; 42 BP.

XX AAQ87144;

XX 24-JAN-1996 (first entry)

DE pBR322 ori downstream amplification primer TG63.

XX Primer; PCR; amplification; recombinant haemoglobin; alpha subunit;
 KW expression vector; purity; beta subunit; tac promoter; tet gene;
 KW lambda repressor gene; lacI; ss.

XX Synthetic.

XX WO9514038-A2.

XX 26-MAY-1995.

XX 15-NOV-1994; 94WO-US013034.

XX 15-NOV-1993; 93US-00153071.

XX (SOMA-) SOMATOGEN INC.

XX Milne EE, Plomer JJ, Rausch SK, Hogenson DC, Ryland JR;
 PI Matthews MH, Ernst UP, Houk DE, Traylor DW, Williams LR;
 PI Mitchell DJ, Chivers ML, Belval TK;

XX WPI; 1995-200344/26.

XX Purification of haemoglobin, esp. recombinant haemoglobin - using e.g.
 PT immobilised metal affinity chromatography heating steps, anion exchange
 PT resins and chelating agents.

XX Example 1; Page 31; 77pp; English.

XX The primers AAQ87135-50 were used to subclone the haemoglobin alpha and
 CC beta genes into bacterial expression vectors. The vectors thus
 CC constructed were used in methods to produce recombinant haemoglobin which
 CC can be purified to pharmaceutically acceptable levels of purity by the
 CC methods of the specification. This primer binds downstream of the pBR322
 CC origin of replication (ori) at pos. 2380-2404. The primer with primer
 CC TG62 (AAQ87143) is used to amplify the pBR322 ori. The ori is used in the
 CC construction of the expression vector pSGE705. This vector contains two
 CC copies of the haemoglobin alpha subunit gene in tandem, linked to the
 CC beta subunit gene, all under control of the tac promoter (AAQ87136-7).
 CC The plasmid also has inserted the tet gene and the lacI gene for
 CC regulation of the production of haemoglobin

SQ Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
 Query Match 69.0%; Score 13.8; DB 2; Length 42;
 Best Local Similarity 88.2%; Pred. No. 8.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGTCAT 20
 Db 16 ACGCTGGCTCGGTCGT 32

RESULT 10

AAT32725

ID AAT32725 standard; DNA; 42 BP.

XX AAT32725;

XX 07-JAN-1997 (first entry)

DE Oligo TG63 for creation of recombinant haemoglobin.

XX Haemoglobin; alpha globin; beta globin; Hb; dietary supplement; anaemia;
 KW molecular weight marker; oxygen carrier; transfusion; oxygen delivery;
 KW erythrocyte; nitric oxide; non-oxygenated ligand; therapy; hypertension;
 KW hypotension; septic shock; polymerase chain reaction; primer; amplify;
 KW PCR; ss.

XX Synthetic.

XX WO9615151-A1.

XX 23-MAY-1996.

XX 11-MAY-1995; 95WO-US005786.

XX 14-NOV-1994; 94US-00339304.

XX 10-MAY-1995; 95US-00438511.

XX (SOMA-) SOMATOGEN INC.

XX Plomer JJ, Ryland JR, Matthews MH, Traylor DW, Milne EE;
 PI Durfee SL, Mathews AJ, Neway JO;

XX WPI; 1996-259784/26.

XX Purificn. of haemoglobin soln. from cell lysate by metal affinity
 PT chromatography - opt. followed by anion exchange chromatography and
 PT oxygenation of the soln., partic. useful as therapeutic oxygen carrier.

XX Example 1; Page 30; 74pp; English.

XX AAT32717-T32725 represent oligonucleotides used in the creation of the
 CC plasmid pSGE705. This sequence represents the downstream primer for the
 CC pBR322 ori. pSGE705 contains the pBR322 ori, a lacI gene, a di-alpha
 CC globin gene, a tetracycline resistance gene, and a beta globin gene. A
 CC lysate of bacteria transformed with pSGE705 is then used in the method of
 CC the invention for production of a haemoglobin (Hb) solution. In the
 CC method, a Hb-containing lysate is applied to an immobilised metal
 CC affinity chromatography resin loaded with a divalent ion. The resin is
 CC washed with a solution containing a competitive ligand, then washed with
 CC a buffer to remove the competitive ligand. The solution is the eluted to
 CC recover a partially purified Hb solution. The Hb solution produced can be
 CC used as dietary supplements to provide iron, as molecular weight markers,
 CC and as oxygen carriers for transfusions. Also, the solution can be used
 CC to treat anaemia, to deliver oxygen to cell cultures or, in vivo, to
 CC tissues downstream of occlusions that cannot be reached by erythrocytes.
 CC The Hb can also function to deliver or remove nitric oxide (NO) or non-
 CC oxygenated ligands, as a drug delivery vehicle, and to remove oxygen from
 CC solutions. The delivery of NO is useful as therapy in cases of
 CC hypertension, while removal of excess NO can be used to treat hypotension
 CC and septic shock. The method can be applied to lysates of erythrocytes,
 CC or of recombinant cells, and is able to remove the large amounts of
 CC contaminants present in recombinant Hb solutions

```
XX SQ Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTTCAT 20
|||||
Db 16 ACGCTGCGCTCGGTTCGT 32

RESULT 11
AAAT73265
ID AAT73265 standard; DNA; 42 BP.
XX
AC AAT73265;
XX
DT 11-SEP-1997 (first entry)
XX
DE Downstream primer TG63 to amplify pBR322 origin of replication.
XX
KW Linker; haemoglobin; alpha domain; beta domain; red blood cell;
KW haemorrhage; trauma; anaemia; surgery; oxygen carrying capacity.
XX
OS Synthetic.
XX
PN WO9640920-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US010420.
XX
PR 07-JUN-1995; 95US-00487431.
XX
PA (SOMA-) SOMATOGEN INC.
XX
PI Trimble SP, Anderson DC, Mathews AJ, Anthony-Cahill S;
PI Marquardt DA, Madril DG, Kerwin BA, Epp JK;
XX
DR WPI; 1997-052322/05.
XX
Globin-like polypeptide comprising 2 di:alpha domains - useful as red
PT blood cell substitute, e.g. in treatment of haemorrhage(s), trauma(s),
PT anaemia(s) and in surgery.
XX
Example 1; Page 21; 61pp; English.
XX
The invention relates to a globin-like polypeptide comprising 2 dialpha
CC domains preferably linked by a peptide linker of 7 or 14 amino acids,
CC such as AAW2221-3, attached to other globin-like molecules, e.g. beta-
CC globin molecules. The primers AAT73264-5 were used to amplify the origin
CC of replication from the plasmid pBR322, in order to construct a plasmid
CC for expression of the novel haemoglobin-like protein. This primer binds
CC to nucleotides 2380-2404 of the ori sequence. The amplified fragment was
CC ligated to a fragment containing the tet resistance gene from plasmid
CC pSELECT-1 (Promega). These fragments were inserted into pUC19 to generate
CC plasmid pSGE507. Into pSGE507, a fragment containing the alpha and beta
CC haemoglobin chains was inserted as was a fragment encoding a linked di-
CC alpha chain. The final construct was named pSGE513. The haemoglobin-like
CC proteins and compositions containing them can be used as red blood cell
CC substitutes, e.g. for treating haemorrhages, traumas, anaemias and
CC surgeries where fluid volume and/or oxygen carrying capacity must be
CC replaced
XX
Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTTCAT 20
|||||
Db 16 ACGCTGCGCTCGGTTCGT 32

RESULT 12
AAT60986
ID AAT60986 standard; DNA; 42 BP.
XX
AC AAT60986;
XX
DT 28-OCT-1997 (first entry)
XX
DE Downstream primer for pBR322 ori positions 2380-2404.
XX
KW Preparation; construction; plasmid; pSGE705; pBR; globin;
KW replication origin; tetracycline resistance; di-alpha; di-beta;
KW tac promoter; lacI; primer; polymerase chain reaction; PCR;
KW amplification; ss.
XX
OS Synthetic.
XX
PN WO9704110-A1.
XX
PD 06-FEB-1997.
XX
PF 12-JUL-1996; 96WO-US011600.
XX
PR 14-JUL-1995; 95US-0001179P.
XX
PA (SOMA-) SOMATOGEN INC.
XX
PI Weickert MJ, Glascock CB;
XX
DR WPI; 1997-132648/12.
XX
Prokaryotic cell contg. plasmid including regulatable expression unit -
PT for heterologous protein, and chromosomal gene encoding regulator of this
PT unit controlled by strong promoter, provides tight control of expression.
XX
Example 1; Page 15; 60pp; English.
XX
The present sequence was used in the preparation of the plasmid pSGE705,
CC which has the pBR origin of replication, tetracycline resistance gene,
CC the di-alpha and di-beta globin genes, tac promoter and lacI
XX
Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTTCAT 20
|||||
Db 16 ACGCTGCGCTCGGTTCGT 32

RESULT 13
AAV58346
ID AAV58346 standard; DNA; 42 BP.
XX
AC AAV58346;
XX
DT 20-NOV-1998 (first entry)
XX
DE Primer TG63 for haemoglobin mutant coding sequence.
XX
KW PCR primer; haemoglobin mutant; N-terminal methylation; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN US5811264-A.
XX
PD 22-SEP-1998.
```

XX 29-FEB-1996; 96US-00609271.
 XX 27-JAN-1994; 94US-00188374.
 XX (SOMA-) SOMATOGEN INC.
 XX Levine JD, Aitken JF, Apostol IZ, Lippincott JA;
 XX WPI; 1998-530871/45.
 XX Mutated protein without proline at position 4 - to eliminate N-terminal
 XX methylation.
 XX Example 1; Col 15; 26pp; English.
 XX This sequence represents a primer for a mutated haemoglobin of the
 XX invention. The invention relates to a mutated variant of a protein that
 XX has proline at position 4 and is at least partially methylated on its N
 XX terminus when expressed in bacteria, the variant has an amino acid other
 XX than proline at position 4 and is not methylated on its N-terminus when
 XX expressed in bacteria. Recombinant haemoglobin that is not N-terminally
 XX methylated might avoid the immunological consequences implied by such
 XX methylation
 XX
 XX Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
 Query Match 69.0%; Score 13.8; DB 2; Length 42;
 Best Local Similarity 88.2%; Pred. No. 8.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 ACGGGCGCTCGGTGCAT 20
 Db 16 ACGTGGCGCTCGGTGCT 32
 RESULT 14
 AAC81485
 ID AAC81485 standard; DNA; 42 BP.
 XX
 XX AAC81485;
 XX
 XX 28-FEB-2001 (first entry)
 XX pBR322 ori downstream PCR primer, SEQ ID NO:21.
 XX Recombinant human haemoglobin; rhb1.1; bacterial expression;
 XX N-terminal methionine methylation signal; demethylation;
 XX Escherichia coli; non-immunogenic; pharmaceutical composition;
 XX PCR primer; ss.
 XX Synthetic.
 XX OS
 XX US6140071-A.
 XX 31-OCT-2000.
 XX 27-JAN-1994; 94US-00188374.
 XX 27-JAN-1994; 94US-00188374.
 XX (SOMA-) SOMATOGEN INC.
 XX Aitken JF, Apostol IZ, Levine JD, Lippincott JA;
 XX WPI; 2001-048957/06.
 XX Decreasing methylation of an N-terminus protein, especially hemoglobin
 XX having proline at amino acid position 4, useful for producing
 XX demethylated proteins for treating diseases, by altering this amino acid
 XX to a non-proline residue.
 XX Example 1; Col 15; 26pp; English.

XX The invention relates to a method of decreasing the amount of N-terminal
 XX methionine methylation on a protein expressed in a bacterium. The
 XX bacterial methyltransferase which directs N-terminal methionine
 XX methylation recognises proteins which have a proline residue at position
 XX 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis
 XX protein CheZ). The method comprises introducing mutations into the DNA
 XX encoding the protein so that residue 4 is a non-proline residue, thereby
 XX reducing the degree of N-terminal methylation when the protein is
 XX expressed in a bacterium. The method is useful for decreasing methylation
 XX of a protein, particularly a recombinantly produced protein. The
 XX demethylated protein can be used in a pharmaceutical composition for the
 XX treatment of a disease but with less likelihood of eliciting an
 XX immunological response. These demethylated proteins may be used as
 XX therapeutic agent for the treatment and/or amelioration of disease or
 XX symptoms associated with a disease. The exemplifications describe the
 XX expression of a recombinant human haemoglobin construct (rhb1.1) in
 XX Escherichia coli, and its modification such that residue 4 of the di-
 XX alpha chain of the recombinant haemoglobin is altered from proline to a
 XX non-proline residue. The present sequence represents a PCR primer used in
 XX the exemplifications of the invention
 XX
 XX Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
 Query Match 69.0%; Score 13.8; DB 5; Length 42;
 Best Local Similarity 88.2%; Pred. No. 8.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 ACGGGCGCTCGGTGCAT 20
 Db 16 ACGTGGCGCTCGGTGCT 32
 RESULT 15
 ACI03862/C
 ID ACI03862 standard; DNA; 25 BP.
 XX
 XX ACI03862;
 XX
 XX 13-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 3853.
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 XX genetic variation; biallelic marker; polymorphism; human;
 XX cross-species comparison.
 XX OS
 XX Homo sapiens.
 XX US2003104410-A1.
 XX 05-JUN-2003.
 XX 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-0276759P.
 XX (AFFY-) AFFYMETRIX INC.
 XX Mittmann MP;
 XX WPI; 2003-567953/53.
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 XX Southern, Northern or dot-blot hybridization to identify or detect the
 XX sequence or specific mutations of any gene.
 XX Claim 1; SEQ ID NO 3853; 9pp; English.
 XX The invention discloses a microarray comprising a plurality of nucleic
 XX acid probes including one of 2,018,500 fully defined sequences, or its
 XX perfect match, perfect mismatch, antisense match or antisense mismatch.
 XX Also disclosed is a method of gene expression analysis. The array is used

CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGACGGGGCGCTCGGTCA 19
Db 24 GGACTCGTCGGTCGTCA 7

Search completed: December 13, 2005, 13:29:55
Job time : 263 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:30:55 ; Search time 1918 Seconds
(without alignments)
487.874 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_hic:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_ges1:*
- 10: gb_ges2:*
- 11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	13.6	68.0	49	7 CO780197	CO780197 BL009A.A0
3	13.4	67.0	49	3 B1760726	B1760726 603044726
4	13.2	66.0	37	2 B166786	B166786 602339133
5	13.2	64.0	32	2 BF131807	BF131807 601820724
6	12.8	64.0	42	3 B1553162	B1553162 603197760
7	12.8	64.0	50	1 AU105403	AU105403 AU105403
8	12.8	64.0	50	1 AU105404	AU105404 AU105404
9	12.8	64.0	50	1 AU105405	AU105405 AU105405
10	12.8	64.0	50	1 AU105406	AU105406 AU105406
11	12.6	63.0	50	1 AU107987	AU107987 AU107987
12	12.6	63.0	50	1 AU107995	AU107995 AU107995
13	12.4	62.0	26	10 AG203073	AG203073 Pan trogl
14	12.4	62.0	50	1 AU105647	AU105647 AU105647
15	12.4	62.0	50	1 AU105649	AU105649 AU105649
16	12.2	61.0	28	1 A1287864	A1287864 gv07d12.x
17	12.2	61.0	38	2 BF525570	BF525570 602069675
18	12.2	61.0	45	9 A026252	A026252 1(3)L3130
19	12.2	61.0	50	1 AU107551	AU107551 AU107551
20	12	60.0	31	1 A8867755	A8867755 vx16b08.r
21	12	60.0	41	10 CZ169504	CZ169504 G050C04.G
22	12	60.0	49	1 A1339668	A1339668 qk63cl2.x

23	12	60.0	50	1	AU104529	AU104529
24	12	60.0	50	1	AU104530	AU104530
25	12	60.0	50	1	AU105685	AU105685
26	11.8	59.0	37	1	AA765049	AA765049 n278b02.8
27	11.8	59.0	40	9	CC940970	CC940970 01S0630-0
28	11.8	59.0	45	9	BH913356	BH913356 3526 1.39
29	11.8	59.0	47	10	CL639088	CL639088 G080A08.G
30	11.8	59.0	48	9	CC183531	CC183531 XE344 Bay
31	11.8	59.0	49	10	CL212525	CL212525 G043F09.G
32	11.8	59.0	50	1	AU102922	AU102922 AU102922
33	11.8	59.0	50	1	AU104465	AU104465 AU104465
34	11.8	59.0	50	1	AU106742	AU106742 AU106742
35	11.6	58.0	36	11	DR31K11T	DR31K11T
36	11.6	58.0	38	6	CF296430	CF296430 30DGS---06
37	11.6	58.0	42	10	CL301794	CL301794 P002A12.G
38	11.6	58.0	43	7	CV066602	CV066602 WNE16a11
39	11.6	58.0	44	9	AZ875839	AZ875839 2M0190006
40	11.6	58.0	50	1	AU102349	AU102349 AU102349
41	11.6	58.0	50	1	AU102706	AU102706 AU102706
42	11.6	58.0	50	1	AU104699	AU104699 AU104699
43	11.6	58.0	50	1	AU104786	AU104786 AU104786
44	11.6	58.0	50	1	AU104787	AU104787 AU104787
45	11.6	58.0	50	1	AU104788	AU104788 AU104788

ALIGNMENTS

RESULT 1
BM050289
LOCUS 603632506F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5423352 5',
DEFINITION mRNA sequence.
ACCESSION BM050289
VERSION BM050289.1 GI:16779556
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 36)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCMi882 row: k column: 01
High quality sequence stop: 33.
Location/Qualifiers
1. .36
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5423352"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site:1; XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

FEATURES
source

```

ORIGIN
Query Match      69.0%; Score 13.8; DB 3; Length 36;
Best Local Similarity 88.2%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGT 17
    ||| ||||| |||
Db 19 GGGCGCGGCGCTCGGT 35

RESULT 2
CO780197
LOCUS
DEFINITION
BL009A A05 6-Day Axolotl Tail Blastema (6DaxBL) Ambystoma mexicanum
cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION
CO780197
VERSION
CO780197.1 GI:50996177
KEYWORDS
EST.
SOURCE
Ambystoma mexicanum (axolotl)
ORGANISM
Ambystoma mexicanum
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 49)
Haber mann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Protenhauerstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL009A row: 05 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1..49
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:9296"
/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH108-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DaxBL"

ORIGIN
Query Match      68.0%; Score 13.6; DB 7; Length 49;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGT CAT 20
    ||| ||||| ||||| |||
Db 7 GGGCAGCGGTCTCGGT CAT 26

RESULT 3
BI760726
LOCUS
DEFINITION
G03044726F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185086 5',
mRNA sequence.
ACCESSION
BI760726
VERSION
BI760726.1 GI:15752304

ORIGIN
Query Match      67.0%; Score 13.4; DB 3; Length 49;
Best Local Similarity 93.3%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGGGCGCTCGGTC 18
    ||| ||||| ||||| |||
Db 31 AAGCGGGCGCTCGGTC 45

RESULT 4
BG166786
LOCUS
DEFINITION
BG166786 602339133F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4446993 5',
mRNA sequence.
ACCESSION
BG166786
VERSION
BG166786.1 GI:12673489
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 37)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

ORIGIN
Query Match      67.0%; Score 13.4; DB 3; Length 49;
Best Local Similarity 93.3%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGGGCGCTCGGTC 18
    ||| ||||| ||||| |||
Db 31 AAGCGGGCGCTCGGTC 45

RESULT 4
BG166786
LOCUS
DEFINITION
BG166786 602339133F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4446993 5',
mRNA sequence.
ACCESSION
BG166786
VERSION
BG166786.1 GI:12673489
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 37)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```


Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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High quality sequence stop: 37.

FEATURES

source

1. .37

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4446993"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 66.0%; Score 13.2; DB 2; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACCGCGCTCGTTC 18
Db 12 GGAACCGCGCTCGTTC 29

RESULT 5

BF131807/c

LOCUS BF131807 32 bp mRNA linear EST 24-OCT-2000
DEFINITION 60182072F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052596 5', mRNA sequence.

ACCESSION BF131807.1 GI:10970847

VERSION EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 32)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs@email.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LICM889 row: p column: 05

High quality sequence start: 8

High quality sequence stop: 30.

FEATURES

source

1. .32

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/clone="IMAGE:4052596"
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/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_58"
/notes="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 32;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGCGCGCTCGTCAT 20
Db 27 CGCTGCGCTCGTCGT 12

RESULT 6

BI553162

LOCUS BI553162 42 bp mRNA linear EST 05-SEP-2001
DEFINITION 603197760F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277350 5', mRNA sequence.

ACCESSION BI553162

VERSION BI553162.1 GI:154440474

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 42)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs@email.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11700 row: g column: 15

High quality sequence stop: 42.

FEATURES

source

1. .42

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5277350"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/notes="Organ: Brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 64.0%; Score 12.8; DB 3; Length 42;
Best Local Similarity 87.5%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACCGCGCTCGG 16
| | | | | | | | | | | | | | | |

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Db      8 GGACGGCGGAGCTCGG 23

RESULT 7
AUI05403/c
LOCUS   AUI05403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
CAS05957, mRNA sequence.
ACCESSION AUI05403.1 GI:13554924
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
PUBMED   11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
     source            1..50
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGACGGCGGCTCGGT 17
        ||||| |||||
Db      48 GGACGGCGGCTCGCT 33

RESULT 9
AUI05405/c
LOCUS   AUI05405 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
ZRV61110, mRNA sequence.
ACCESSION AUI05405
VERSION   AUI05405.1 GI:13554926
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
PUBMED   11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGACGGCGGCTCGGT 17
        ||||| |||||
Db      42 GGACGGCGGCTCGCT 27

RESULT 8
AUI05404/c
LOCUS   AUI05404 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
HRC10340, mRNA sequence.
ACCESSION AUI05404
VERSION   AUI05404.1 GI:13554925
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
PUBMED   11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGACGGCGGCTCGGT 17
        ||||| |||||
Db      42 GGACGGCGGCTCGCT 27

RESULT 8
AUI05404/c
LOCUS   AUI05404 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
HRC10340, mRNA sequence.
ACCESSION AUI05404
VERSION   AUI05404.1 GI:13554925
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
PUBMED   11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGACGGCGGCTCGGT 17
        ||||| |||||
Db      42 GGACGGCGGCTCGCT 27

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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             Location/Qualifiers
     source            1..50
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGACGGCGGCTCGGT 17
        ||||| |||||
Db      48 GGACGGCGGCTCGCT 33

RESULT 9
AUI05405/c
LOCUS   AUI05405 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
ZRV61110, mRNA sequence.
ACCESSION AUI05405
VERSION   AUI05405.1 GI:13554926
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
PUBMED   11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
     source            1..50
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      64.0%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGACGGCGGCTCGGT 17
        ||||| |||||
Db      42 GGACGGCGGCTCGCT 27

```

RESULT 10
 AUI05406/c
 LOCUS
 DEFINITION AUI05406 Sugano Homo sapiens cDNA library EST 28-JAN-2004
 AUI05406.1 mRNA linear
 AUI05406.1 mRNA sequence.
 AUI05406.1 GI:13554927

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
 Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL
 PUBMED
 COMMENT

EMBO Rep. 2 (5), 388-393 (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezuki@ims.u-tokyo.ac.jp

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="ADSE01811"

/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 64.0%; Score 12.8; DB 1; Length 50;

Best Local Similarity 87.5%; Pred. No. 2.3e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGT 17

Db 16 GGACGGCGCGCTCGGT 1

RESULT 11

AUI07987/c

LOCUS

DEFINITION AUI07987 Sugano Homo sapiens cDNA library EST 28-JAN-2004

AUI07987.1 mRNA linear

AUI07987.1 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezuki@ims.u-tokyo.ac.jp

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CAS04356"

/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 63.0%; Score 12.6; DB 1; Length 50;

Best Local Similarity 78.9%; Pred. No. 2.9e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCA 19

Db 49 GGGCGCGCGCGCGCGACA 31

RESULT 12

AUI07995/c

LOCUS

DEFINITION AUI07995 Sugano Homo sapiens cDNA library EST 28-JAN-2004

AUI07995.1 mRNA linear

AUI07995.1 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezuki@ims.u-tokyo.ac.jp

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KAIA2600"

/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 63.0%; Score 12.6; DB 1; Length 50;

Best Local Similarity 78.9%; Pred. No. 2.9e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCA 19

Db 45 GGGCGCGCGCGCGCGACA 27

RESULT 13

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AG203073      26 bp   DNA       linear   GSS 06-MAR-2004
LOCUS         Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey
DEFINITION
ACCESSION    AG203073
VERSION      AG203073.1 GI:452335248
KEYWORDS     GSS.
SOURCE       Pan troglodytes (chimpanzee)
ORGANISM     Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE    1
AUTHORS      Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE        BAC end sequences of Library RP-43
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 26)
AUTHORS      Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE        Direct Submission
JOURNAL      Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
[8-mail:redstone@mail.krribb.re.kr, URL:http://phs.grc.krribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409]
COMMENT      Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector       : pBACe3.6
R.Site 1     : EcoRI.
R.Site 2     : EcoRI.
Location/Qualifiers
1. .26
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-087B01.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match      62.0%; Score 12.4; DB 10; Length 26;
Best Local Similarity 92.9%; Pred. No. 3.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGACGCGGCGCTC 14
        ||||| |||||
Db      1 GGGACTCGGCGCTC 14

RESULT 14
LOCUS         AU105647/c      50 bp   mRNA       linear   EST 28-JAN-2004
DEFINITION    AU105647 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HS100961, mRNA sequence.
ACCESSION    AU105647
VERSION      AU105647.1 GI:13555168
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS102850"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      62.0%; Score 12.4; DB 1; Length 50;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGACGCGGCGCTC 14
        ||||| |||||
Db      1 GGGACTCGGCGCTC 14

RESULT 15
LOCUS         AU105649/c      50 bp   mRNA       linear   EST 28-JAN-2004
DEFINITION    AU105649 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HS102850, mRNA sequence.
ACCESSION    AU105649
VERSION      AU105649.1 GI:13555170
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS102850"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      62.0%; Score 12.4; DB 1; Length 50;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGACGCGGCGCTC 14
        ||||| |||||
Db      1 GGGACTCGGCGCTC 14

```

```

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS100961"
/clone_lib="Sugano Homo sapiens cDNA library"
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Query Match      62.0%; Score 12.4; DB 1; Length 50;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGACGCGGCGCTC 14
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Db      1 GGGACGCGGCGCTC 4

RESULT 15
LOCUS         AU105649/c      50 bp   mRNA       linear   EST 28-JAN-2004
DEFINITION    AU105649 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HS102850, mRNA sequence.
ACCESSION    AU105649
VERSION      AU105649.1 GI:13555170
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS102850"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      62.0%; Score 12.4; DB 1; Length 50;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGACGCGGCGCTC 14
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Db      1 GGGACGCGGCGCTC 4

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Qy 1 GGGACGGGGGCTC 14
Db 17 GTGACGGGGGCTC 4

Search completed: December 13, 2005, 14:30:26
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:16:54 ; Search time 94 Seconds
(without alignments)
378.205 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	13.8	69.0	25	3	US-09-396-196G-46323
C 4	13.8	69.0	25	3	US-09-396-196G-46324
C 5	13.8	69.0	25	3	US-09-396-196G-46335
6	13.8	69.0	42	2	US-08-153-071-14
7	13.8	69.0	42	2	US-08-609-271-21
8	13.8	69.0	42	2	US-08-438-511-14
9	13.8	69.0	42	2	US-08-487-431-17
10	13.8	69.0	42	3	US-08-188-374-21
11	13.8	69.0	42	3	US-08-973-629-17
12	13.2	66.0	25	3	US-09-396-196G-53301
13	13	65.0	20	3	US-09-046-858A-19
14	13	65.0	20	3	US-09-450-515-19
15	13	65.0	20	3	US-10-206-654-19
C 16	12.8	64.0	37	3	US-08-944-410-47
C 17	12.8	64.0	40	2	US-08-425-684-86
C 18	12.8	64.0	40	2	US-08-425-684-128
C 19	12.8	64.0	40	2	US-08-675-502-86
C 20	12.8	64.0	40	2	US-08-675-502-128
C 21	12.8	64.0	40	3	US-09-245-802-86
C 22	12.8	64.0	40	3	US-09-245-802-128
C 23	12.6	63.0	20	3	US-09-131-827-8773
C 24	12.6	63.0	24	3	US-10-540-014-35

Sequence 12, Appl
Sequence 14, Appl
Sequence 35, Appl
Sequence 40648, A
Sequence 52, Appl
Patent No. 5240848
Sequence 9, Appl
Sequence 30, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 9, Appl
Sequence 41065, A
Sequence 46162, A
Sequence 46163, A
Sequence 9, Appl
Sequence 38, Appl
Sequence 58, Appl
Sequence 62, Appl
Sequence 25195, A
Sequence 49392, A
Sequence 3, Appl

US-09-164-210-12
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US-10-091-841A-35
US-09-396-196G-40648
US-09-319-648-52
5240848-8
US-08-943-915-30
US-08-182-175A-9
US-08-474-633A-16
US-08-823-771-16
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US-09-396-196G-41065
US-09-396-196G-46162
US-09-396-196G-46163
US-08-753-054-9
US-09-158-863C-38
US-09-589-560B-58
US-09-589-560B-62
US-09-396-196G-25195
US-09-396-196G-49392
US-09-487-558B-3

ALIGNMENTS

RESULT 1
US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Patent No. 6750042
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCA 19
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Db 6 GGGCTCGGGCTCGGGCA 24

RESULT 2
US-09-396-196G-42173/C
; Sequence 42173, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42173

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Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGGCGCTCGGTTCAT 20
DB 20 CGGCGCTCGGTTCAT 7
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RESULT 3
US-09-396-196G-46323/c
; Sequence 46323, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46323

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Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
DB 20 ACGCTGCGCACGGTTCAT 4
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RESULT 4
US-09-396-196G-46324/c
; Sequence 46324, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46324

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Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
DB 19 ACGCTGCGCACGGTTCAT 3
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; Sequence 46335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46335

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Best Local Similarity 88.2%; Pred. No. 4.6e+03;
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QY 4 ACGCGCGCTCGGTTCAT 20
DB 18 ACGCTGCGCACGGTTCAT 2
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RESULT 6
US-08-153-071-14
; Sequence 14, Application US/08153071
; Patent No. 5665869
; GENERAL INFORMATION:

; APPLICANT: Ryland, James R.
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Ernst, Ulrich P.
; APPLICANT: Houk, Daniel E.
; APPLICANT: Traylor, David W.
; APPLICANT: Williams, Lee R.
; APPLICANT: Mitchell, David J.
; APPLICANT: Chivers, Mark L.
; APPLICANT: Belval, Thomas K.
; TITLE OF INVENTION: Method for the Rapid Removal of
; PROTOPORPHYRIN IX from Protoporphyrin IX-Containing Solutions
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,071
; FILING DATE: No. 5665869ember 15, 1993
; CLASSIFICATION: 530


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ATTORNEY/AGENT INFORMATION:
; NAME: No. 565869ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer for pBR322 ori positions
; MOLECULE TYPE: 2380-2404
; HYPOTHETICAL: no
US-08-153-071-14

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Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGCGCTCGGTGCAT 20
Db 16 ACGTGCCTCGGTGCT 32

RESULT 7
US-08-609-271-21
; Sequence 21, Application US/08609271
; Patent No. 5811264
; GENERAL INFORMATION:
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Apostol, Izidor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylatic
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Site FD-1
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,271
; FILING DATE: 28 February 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,374
; FILING DATE: 1/27/94
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5811264elli, Marianne F.
; REGISTRATION NUMBER: 38571
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32547
; REFERENCE/DOCKET NUMBER: 170/div
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3324
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
; HYPOTHETICAL: no
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US-08-609-271-21

Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGCGCTCGGTGCAT 20
Db 16 ACGTGCCTCGGTGCT 32

RESULT 8
US-08-438-511-14
; Sequence 14, Application US/08438511
; Patent No. 5840851
; GENERAL INFORMATION:
; APPLICANT: Plomer, J. Jeffrey
; APPLICANT: Ryland, James R.
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Traylor, David W.
; APPLICANT: Milne, Erin E.
; APPLICANT: Durfee, Steven L.
; APPLICANT: Mathews, Antony J.
; APPLICANT: Neway, Justin O.
; TITLE OF INVENTION: Purification of Hemoglobin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Suite FDI
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,511
; FILING DATE: 10 May 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/339,304
; FILING DATE: No. 5840851ember 14, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,273
; FILING DATE: July 23, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5840851elli, Marianne F.
; REGISTRATION NUMBER: 38571
; REFERENCE/DOCKET NUMBER: 191
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3324
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
; HYPOTHETICAL: no
US-08-438-511-14

Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGCGCTCGGTGCAT 20
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Db      16  ACGTCGGCTCGGTCT 32
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RESULT 9
US-08-487-431-17
; Sequence 17, Application US/08487431
; Patent No. 5844090
; GENERAL INFORMATION:
; APPLICANT: Anderson, David C.
; APPLICANT: Mathews, Antony J.
; APPLICANT: Trimble, Stephen P.
; APPLICANT: Anthony-Cahill, Spencer
; TITLE OF INVENTION: Modified Hemoglobin-like Compounds
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Suite FD1
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,431
; FILING DATE: June 7, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,712
; FILING DATE: No. 5844090ember 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 61
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramsey R. Stewart
; REGISTRATION NUMBER: 38,322
; REFERENCE/DOCKET NUMBER: 61
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3356
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
; HYPOTHETICAL: no
; US-08-487-431-17
Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4  ACGCGCGCTCGGTCTAT 20
Db      16  ACGTCGGCTCGGTCT 32
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RESULT 10
US-08-188-374-21
; Sequence 21, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aiken F., Jacqueline
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth
; FILE REFERENCE: 3101.1
; FILE REFERENCE: BXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; CURRENT FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer for
; OTHER INFORMATION: pBR32 ori positions 2380-2404
; US-08-188-374-21
Query Match 69.0%; Score 13.8; DB 3; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4  ACGCGCGCTCGGTCTAT 20
Db      16  ACGTCGGCTCGGTCT 32
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RESULT 11
US-08-973-629-17
; Sequence 17, Application US/08973629A
; Patent No. 6150506
; GENERAL INFORMATION:
; APPLICANT: Trimble, Stephen
; APPLICANT: Mathews, Anthony
; APPLICANT: Kerwin, Bruce
; APPLICANT: Marguardt, David
; APPLICANT: Anthony-Cahill, Spencer
; APPLICANT: Epp, Janice
; APPLICANT: Madril, Dominic
; APPLICANT: Anderson, David
; TITLE OF INVENTION: MODIFIED HEMOGLOBIN-LIKE COMPOUNDS AND METHODS OF
; TITLE OF INVENTION: PURIFYING SAME
; FILE REFERENCE: BXTB 1928
; CURRENT APPLICATION NUMBER: US/08/973,629A
; CURRENT FILING DATE: 1998-08-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide or 3' primer for generation of
; OTHER INFORMATION: pBR322 ori with PmeI site
; US-08-973-629-17
Query Match 69.0%; Score 13.8; DB 3; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4  ACGCGCGCTCGGTCTAT 20
Db      16  ACGTCGGCTCGGTCT 32
||||| ||||||||| |||
RESULT 12
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
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; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53301

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCGTGCAT 20
||| ||||| |||||
Db 2 GACCCAGCGCTCTGTCAT 19

RESULT 13
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/046.858A

FILING DATE: 24-MAR-1998

CLASSIFICATION: 800

PRIOR APPLICATION NUMBER: 60/042,376

FILING DATE: 24-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Dehlinger, Peter J.

REGISTRATION NUMBER: 28,006

REFERENCE/DOCKET NUMBER: 2000-0456.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960

TELEX:

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-046-858A-19

Query Match 65.0%; Score 13; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCG 15

||||| ||||| |||||

Db 2 GACGCGGCGCTCG 14

RESULT 14
US-09-450-515-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/450.515

FILING DATE: 29-No. 6680425-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/046.858

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Dehlinger, Peter J.

REGISTRATION NUMBER: 28,006

REFERENCE/DOCKET NUMBER: 2000-0456.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-450-515-19

Query Match 65.0%; Score 13; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCG 15

||||| ||||| |||||

Db 2 GACGCGGCGCTCG 14

||||| ||||| |||||

RESULT 15

US-10-206-654-19

; Sequence 19, Application US/10206654

; Patent No. 6919493

; GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond L.

; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES

; IN ALPHA-AMYLASE GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: PO Box 60850

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

Query Match      65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GACGCGCGCTCG 15
        |||||
Db      2 GACGCGCGCTCG 14

Search completed: December 13, 2005, 14:32:05
Job time : 95 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:25:43 ; Search time 445 Seconds
(without alignments)
371.657 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	7	US-10-605-498-82
2	20	100.0	21	7	US-10-605-498-81
3	19	95.0	19	7	US-10-605-498-90
4	16	80.0	21	7	US-10-605-498-3
5	15.2	76.0	25	7	US-10-719-956-135321
6	15	75.0	21	7	US-10-605-498-4
7	14.2	71.0	25	10	US-11-036-317-261850
8	14.2	71.0	25	10	US-11-036-317-269817
9	14.2	71.0	25	10	US-11-036-317-330516
10	14.2	71.0	25	10	US-11-036-317-332488
11	14.2	71.0	25	10	US-11-036-317-364465
12	14.2	71.0	25	10	US-11-036-317-406575
13	14.2	71.0	25	10	US-11-036-317-536426
14	14.2	71.0	25	10	US-11-036-317-536427
15	14.2	71.0	33	3	US-09-977-137A-16
16	14	70.0	25	5	US-10-215-112-7242
17	14	70.0	25	9	US-10-809-189-42173
18	13.8	69.0	25	9	US-10-809-189-46323
19	13.8	69.0	25	9	US-10-809-189-46324
20	13.8	69.0	25	9	US-10-809-189-46335
21	13.6	68.0	25	7	US-10-719-956-135322
22	13.6	68.0	25	7	US-10-719-956-198103
23	13.6	68.0	25	8	US-10-719-900-309243

24	13.6	68.0	25	10	US-11-036-317-912027	Sequence 912027,
25	13.6	68.0	25	10	US-11-036-317-912041	Sequence 912041,
c 26	13.2	66.0	25	5	US-10-098-263B-3853	Sequence 3853, Ap
27	13.2	66.0	25	5	US-10-098-263B-65789	Sequence 65789, A
28	13.2	66.0	25	7	US-10-719-956-110491	Sequence 110491,
c 29	13.2	66.0	25	7	US-10-719-956-547822	Sequence 547822,
30	13.2	66.0	25	7	US-10-719-956-547823	Sequence 547823,
31	13.2	66.0	25	8	US-10-719-900-148603	Sequence 148603,
32	13.2	66.0	25	8	US-10-719-900-849503	Sequence 849503,
33	13.2	66.0	25	8	US-10-719-900-849504	Sequence 849504,
34	13.2	66.0	25	9	US-10-809-189-53301	Sequence 53301, A
35	13.2	66.0	25	10	US-11-036-317-321539	Sequence 321539,
36	13.2	66.0	25	10	US-11-036-317-787134	Sequence 787134,
c 37	13.2	66.0	25	10	US-11-060-756-166335	Sequence 166335,
c 38	13.2	66.0	25	10	US-11-060-756-166384	Sequence 166384,
c 39	13.2	66.0	25	10	US-11-060-756-229339	Sequence 229339,
c 40	13.2	66.0	25	10	US-11-060-756-229340	Sequence 229340,
41	13.2	66.0	43	3	US-09-792-630-48	Sequence 48, Appl
42	13.2	66.0	43	3	US-09-953-351-48	Sequence 48, Appl
43	13.2	66.0	43	5	US-10-080-376-48	Sequence 48, Appl
44	13.2	66.0	43	5	US-10-082-671-54	Sequence 54, Appl
45	13.2	66.0	43	5	US-10-097-100-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-10-605-498-82
; Sequence 82, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION: Martin
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: USC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; CURRENT FILING DATE: 2003-10-02
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-605-498-82

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTGCAT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGACGGCGCTCGGTGCAT 20

RESULT 2
US-10-605-498-81
; Sequence 81, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION: Martin
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: USC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498

; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-81

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
|||||
DB 2 GGGACGGCGGCTCGGTGCAT 21
|||||

RESULT 3

US-10-605-498-90/c
; Sequence 90, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-605-498-90

Query Match 95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 17; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTGCAT 20
|||||
DB 19 GGACGGCGGCTCGGTGCAT 1
|||||

RESULT 4

US-10-605-498-3
; Sequence 3, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18

; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-3

Query Match 80.0%; Score 16; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGCGCGGCTCGGTGCAT 20
|||||
DB 1 CGCGCGGCTCGGTGCAT 16
|||||

RESULT 5

US-10-719-956-135321/c
; Sequence 135321, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-135321

Query Match 76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
|||||
DB 25 GGGACCGCAACGCTCGGCCAT 6
|||||

RESULT 6

US-10-605-498-4
; Sequence 4, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-4

Query Match 75.0%; Score 15; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCG 15
Db 7 GGGACGGCGCGCTCG 21

RESULT 7

US-11-036-317-261850
; Sequence 261850, Application US/11036317
; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 261850

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-261850

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGTCA 19
Db 3 GGGACGGCGCGATCTGCCA 21

RESULT 8

US-11-036-317-269817

; Sequence 269817, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 269817

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-269817

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGTCA 19
Db 5 GGGACGGCGCGATCTGCCA 23

RESULT 9

US-11-036-317-330516

; Sequence 330516, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 330516

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-330516

; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 330516

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-330516

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGTCA 19
Db 1 GGGACGGCGCGATCTGCCA 19

RESULT 10

US-11-036-317-332488

; Sequence 332488, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 332488

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-332488

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGTCA 19
Db 2 GGGACGGCGCGATCTGCCA 20

RESULT 11

US-11-036-317-364465

; Sequence 364465, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 364465

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-364465

US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
|||||
Db 4 GGGACGGCGGCTCGGTCA 22

RESULT 12

US-11-036-317-406575
Sequence 406575, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036.317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 406575

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
|||||
Db 7 GGGACGGCGGCTCGGTCA 25

RESULT 13

US-11-036-317-536426

Sequence 536426, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036.317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 536426

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
|||||
Db 7 GGGACGGCGGCTCGGTCA 25

RESULT 14

US-11-036-317-536427

Sequence 536427, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036.317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 536427

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
|||||
Db 7 GGGACGGCGGCTCGGTCA 25

RESULT 15

US-09-977-137A-16

Sequence 16, Application US/09977137A

Publication No. US20030104524A1

GENERAL INFORMATION:

APPLICANT: Summers, Anne O.

APPLICANT: Caguiat, Jonathan

TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and

FILE REFERENCE: 79-00

CURRENT APPLICATION NUMBER: US/09/977,137A

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/240,465

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 33

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
|||||
Db 6 GGGCTCGGCGCTCGGGCA 24

Search completed: December 13, 2005, 14:39:40

Job time : 446 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:30:05 ; Search time 144 Seconds
(without alignments)
51.924 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 99gacg9cgctcggtcat 20

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6638722

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.8	64.0	19	8	US-11-101-244-1008030 Sequence 1008030,
C 2	12.8	64.0	19	9	US-11-083-784-1008030 Sequence 1008030,
C 3	12.6	63.0	19	8	US-11-101-244-899787 Sequence 899787,
C 4	12.6	63.0	19	9	US-11-083-784-899787 Sequence 899787,
C 5	12.4	62.0	32	6	US-10-939-294A-16099 Sequence 16099, A
C 6	12.2	61.0	22	7	US-11-176-795-58 Sequence 58, Appl
C 7	12.2	61.0	22	7	US-11-176-795-62 Sequence 62, Appl
C 8	12.2	61.0	32	6	US-10-939-294A-15630 Sequence 15630, A
C 9	12	60.0	19	8	US-11-101-244-877585 Sequence 877585,
C 10	12	60.0	19	9	US-11-083-784-877585 Sequence 877585,
C 11	12	60.0	27	7	US-11-075-046-4 Sequence 4, Appl
C 12	12	60.0	32	7	US-11-075-046-30 Sequence 30, Appl
C 13	11.8	59.0	19	8	US-11-101-244-367704 Sequence 367704,
C 14	11.8	59.0	19	8	US-11-101-244-367714 Sequence 367714,
C 15	11.8	59.0	19	8	US-11-101-244-385820 Sequence 385820,
C 16	11.8	59.0	19	8	US-11-101-244-475963 Sequence 475963,
C 17	11.8	59.0	19	8	US-11-101-244-1128971 Sequence 1128971,
C 18	11.8	59.0	19	8	US-11-101-244-1221629 Sequence 1221629,
C 19	11.8	59.0	19	9	US-11-083-784-367704 Sequence 367704,
C 20	11.8	59.0	19	9	US-11-083-784-367714 Sequence 367714,
C 21	11.8	59.0	19	9	US-11-083-784-385820 Sequence 385820,
C 22	11.8	59.0	19	9	US-11-083-784-475963 Sequence 475963,
C 23	11.8	59.0	19	9	US-11-083-784-1128971 Sequence 1128971,

C 24	11.8	59.0	19	9	US-11-083-784-1221629 Sequence 1221629,
C 25	11.6	58.0	18	6	US-10-231-302-31 Sequence 31, Appl
C 26	11.6	58.0	19	8	US-11-101-244-992967 Sequence 992967,
C 27	11.6	58.0	19	8	US-11-101-244-1512341 Sequence 1512341,
C 28	11.6	58.0	19	8	US-11-101-244-1562938 Sequence 1562938,
C 29	11.6	58.0	19	9	US-11-083-784-992967 Sequence 992967,
C 30	11.6	58.0	19	9	US-11-083-784-1512341 Sequence 1512341,
C 31	11.6	58.0	19	9	US-11-083-784-1562938 Sequence 1562938,
C 32	11.6	58.0	20	7	US-11-069-908-929 Sequence 929, App
C 33	11.6	58.0	20	7	US-11-069-908-3295 Sequence 3295, Ap
C 34	11.6	58.0	32	6	US-10-939-294A-15939 Sequence 15939, A
C 35	11.6	58.0	32	6	US-10-939-294A-16630 Sequence 16630, A
C 36	11.6	58.0	32	6	US-10-939-294A-17166 Sequence 17166, A
C 37	11.6	58.0	32	6	US-10-939-294A-18354 Sequence 18354, A
C 38	11.6	58.0	32	6	US-10-939-294A-18436 Sequence 18436, A
C 39	11.6	58.0	35	6	US-10-525-710-67 Sequence 67, Appl
C 40	11.4	57.0	19	8	US-11-101-244-199478 Sequence 199478,
C 41	11.4	57.0	19	8	US-11-101-244-199517 Sequence 199517,
C 42	11.4	57.0	19	8	US-11-101-244-386259 Sequence 386259,
C 43	11.4	57.0	19	8	US-11-101-244-104567 Sequence 104567,
C 44	11.4	57.0	19	8	US-11-101-244-1436226 Sequence 1436226,
C 45	11.4	57.0	19	9	US-11-083-784-199478 Sequence 199478,

ALIGNMENTS

RESULT 1
US-11-101-244-1008030/c
; Sequence 1008030, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1008030

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GACGCGCGCTCGGTC 18
Db 17 GATGAGCGGTCGCTC 2

RESULT 2
US-11-083-784-1008030/c
; Sequence 1008030, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1008030

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GACGCGCGCTCGGTC 18
||| ||||| |||||
Db 17 GATGAGCGCTCGGTC 2

RESULT 3
US-11-101-244-899787
; Sequence 899787, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 899787
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-899787

Query Match 63.0%; Score 12.6; DB 8; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.2e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGACGCGCGCTCGGTCAT 20
||| ||||| |||||
Db 1 GGAAACGCGCGUGGUCAU 19

RESULT 4
US-11-083-784-899787
; Sequence 899787, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 899787
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-899787

Query Match 63.0%; Score 12.6; DB 9; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.2e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGACGCGCGCTCGGTCAT 20
||| ||||| |||||
Db 1 GGAAACGCGCGUGGUCAU 19

RESULT 5
US-10-939-294A-16099/c
; Sequence 16099, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16099
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16099

Query Match 62.0%; Score 12.4; DB 6; Length 32;
Best Local Similarity 92.9%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGGCTC 14
||| ||||| |||||
Db 21 GGGACGCGCGGCTC 8

RESULT 6
US-11-176-795-58/c
; Sequence 58, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795

; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Coliform Bacteria
US-11-176-795-58

Query Match 61.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGACGGCGCTCGGTC 18
||| ||||| |||||
Db 19 GGATCGCGCTCGGTC 3

RESULT 7
US-11-176-795-62/c
; Sequence 62, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Coliform Bacteria
US-11-176-795-62

Query Match 61.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGACGGCGCTCGGTC 18
||| ||||| |||||
Db 19 GGATCGCGCTCGGTC 3

RESULT 8
US-10-939-294A-15630
; Sequence 15630, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15630
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-15630

Query Match 61.0%; Score 12.2; DB 6; Length 32;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGACGGCGCTCGGTC 18
||| ||||| |||||
Db 8 GGACGGCGACGGCGTC 24

RESULT 9
US-11-101-244-877585/c
; Sequence 877585, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877585
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877585

Query Match 60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCTCGGTCAT 20
||| ||||| |||||
Db 15 GCGCTCGGTCAT 4

RESULT 10
US-11-083-784-877585/c
; Sequence 877585, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877585
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-877585

Query Match 60.0%; Score 12; DB 9; Length 19;

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Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCTCGGTCTCAT 20
Db 15 GCGCTCGGTCTCAT 4

RESULT 11
US-11-075-046-4/c
; Sequence 4, Application US/11075046
; Publication No. US20050268353A1
; GENERAL INFORMATION:
; APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
; TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
; TITLE OF INVENTION: PROTECTING PLANTS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; STREET: DORSEY & WHITNEY LLP
; ADDRESS: FOUR EMBARCADERO CENTER, SUITE 3400
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/075,046
; FILING DATE: 07-MAR-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/677,653
; FILING DATE: 03-Oct-2000
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD F. TRECARTIN
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC
; TELEPHONE: (415) 781-1989
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: CDS
; LOCATION: 6..32
; US-11-075-046-4

Query Match 60.0%; Score 12; DB 7; Length 27;
Best Local Similarity 75.0%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCTCAT 20
Db 20 GCGACGGCGGCTCGGTCTCAT 1

RESULT 12
US-11-075-046-30/c
; Sequence 30, Application US/11075046
; Publication No. US20050268353A1
; GENERAL INFORMATION:
; APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
; TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
; TITLE OF INVENTION: PROTECTING PLANTS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; STREET: DORSEY & WHITNEY LLP
; ADDRESS: FOUR EMBARCADERO CENTER, SUITE 3400
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/075,046
; FILING DATE: 07-MAR-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/677,653
; FILING DATE: 03-Oct-2000
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD F. TRECARTIN
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC
; TELEPHONE: (415) 781-1989
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: CDS
; LOCATION: 6..32
; US-11-075-046-30

Query Match 60.0%; Score 12; DB 7; Length 32;
Best Local Similarity 75.0%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCTCAT 20
Db 25 GCGACGGCGGCTCGGTCTCAT 6

RESULT 13
US-11-101-244-367704/c
; Sequence 367704, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 367704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-367704

Query Match 59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 9.1e+03;

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